WHAT IS CLAIMED IS:

1. An array comprising a nucleic acid component consisting essentially of non-redundant nucleic acid molecules.

2. The array of claim 1, wherein at least about 50 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to an untranslated sequence in an organism.

3. The array of claim 2, wherein said organism is a plant.

4. The array of claim 3, wherein said plant is a corn plant.

5. The array of claim 1, wherein at least about 75 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to an untranslated sequence in an organism.

6. The array of claim 1, wherein at least about 90 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to an untranslated sequence in an organism.

7. The array of claim 1, wherein at least about 95 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to an untranslated sequence in an organism.

8. The array of claim 1, wherein at least about 50 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to a 3' untranslated sequence in an organism.

9. The array of claim 1, wherein at least about 50 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to a 5' untranslated sequence in an organism.

10. The array of claim 1, wherein at least about 50 percent of said non-redundant nucleic acid molecules comprise a nucleic acid sequence corresponding to an intronic sequence in an organism.

11. The array of claim 1, wherein the sequence of each said non-redundant nucleic acid molecule is known.

12. The array of claim 1, wherein said array comprises more than about 500 of said non-redundant nucleic acid molecules.

13. The array of claim 1, wherein said array comprises more than about 1000 of said non-redundant nucleic acid molecules.

14. The array of claim 1, wherein each of said non-redundant nucleic acid molecules comprises a nucleic acid sequence corresponding to a different sequence transcribed in a cell.

15. The array of claim 1, wherein said nucleic acid component comprises at least two groups of non-redundant nucleic acid molecules, wherein each non-redundant nucleic acid molecule within each group comprises a nucleic acid sequence corresponding to a different sequence transcribed in a cell from a source, wherein said source is different for each group.

16. The array of claim 15, wherein said nucleic acid component comprises at least ten of said groups.

17. The array of claim 15, wherein each non-redundant nucleic acid molecule within at least one of said groups comprises a marker such that said source is identifiable.

18. The array of claim 17, wherein said marker is a nucleic acid marker.

19. The array of claim 15, wherein said source is an organ tissue at a stage of development.

20. The array of claim 19, wherein said organ tissue is selected from the group consisting of roots, shoots, stems, leaves, flowers, seeds, and meristems.

21. The array of claim 19, wherein said stage is selected from the group consisting of germinating seedlings, full grown plants, and immature/developing seeds.

22. An IDP primer pair collection comprising at least about 100 different IDP primer pairs, wherein the first primer of each of said IDP primer pair corresponds to a different first sequence within the genome of at least one member of a species, each said different first sequence lacking an IDP for said species, wherein the second primer of each of said IDP primer pairs corresponds to a different second sequence within the genome of at least one member of said species, each said different second sequence containing an IDP for said species.

23. The collection of claim 22, wherein said collection comprises at least about 250 different IDP primer pairs.

24. The collection of claim 22, wherein said collection comprises at least about 500 different IDP primer pairs.

25. The collection of claim 22, wherein said collection comprises at least about 1000 different IDP primer pairs.

26. The collection of claim 22, wherein the sequence of each primer of said collection is known.

27. The collection of claim 22, wherein every fifty cM region of said genome contains at least one of said different first sequences.

28. The collection of claim 22, wherein every twenty-five cM region of said genome contains at least one of said different first sequences.

29. The collection of claim 22, wherein every ten cM region of said genome contains at least one of said different first sequences.

30. The collection of claim 22, wherein every five cM region of said genome contains at least one of said different first sequences.

31. The collection of claim 22, wherein every two cM region of said genome contains at least one of said different first sequences.

32. A method for producing a genetic map for a species, said method comprising:

a) determining a pattern of hybridization products on an array for sets of samples, wherein each sample within a set contains a different collection of fractionated genomic nucleic acid from a member of said species, wherein said member is different for each set, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within the genome of said species, wherein said hybridization products are formed between said nucleic acid molecules and said fractionated genomic nucleic acid, and

b) determining the relationship between said nucleic acid sequences within said genome based on the pattern of hybridization products for each sample of each set and the genetic relationship of said different members for each set, thereby forming said genetic map.

33. The method of claim 32, wherein said species is a plant species.

34. The method of claim 32, wherein said species is maize.

35. The method of claim 32, wherein said sets comprise at least five sets.

36. The method of claim 32, wherein said sets comprise at least ten sets.

37. The method of claim 32, wherein each set comprises at least five samples.

38. The method of claim 32, wherein each set comprises at least ten samples.

39. The method of claim 32, wherein said genomic nucleic acid was digested with at least two restriction enzymes.

40. The method of claim 32, wherein said genomic nucleic acid was digested with at least five restriction enzymes.

41. The method of claim 32, wherein said fractionated genomic nucleic acid is labeled.

42. The method of claim 32, wherein each nucleic acid molecule is unique.

43. The method of claim 32, wherein said array comprises at least about 100 nucleic acid molecules.

44. The method of claim 32, wherein said array comprises at least about 500 nucleic acid molecules.

45. The method of claim 32, wherein said array comprises at least about 1000 nucleic acid molecules.

46. The method of claim 32, wherein every twenty-five cM region of said genome contains at least one of said nucleic acid sequences.

47. The method of claim 32, wherein every two cM region of said genome contains at least one of said nucleic acid sequences.

48. The method of claim 32, wherein said determining the relationship between said nucleic acid sequences within said genome is determining the relative position of said nucleic acid sequences within said genome.

49. The method of claim 32, wherein said determining the relationship between said nucleic acid sequences within said genome is determining the relative distance between said nucleic acid sequences within said genome.

50. A method of producing a genetic map for a species, said method comprising contacting an array with sets of samples, wherein each sample within a set contains a different collection of fractionated genomic nucleic acid from at least one member of said species, said member(s) being different for each set, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within the genome of said species, said contacting being performed such that a pattern of hybridization products is formed for each sample of each set, said hybridization products being formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein the relationship between said nucleic acid sequences within said genome is determinable based on the pattern of hybridization products for each sample of each set and the genetic relationship of said different members for each set, said relationship being said genetic map.

51. A method for identifying a region of a genome of a species, said region containing a nucleic acid sequence that contributes to a phenotype observed in at least one member of said species, said method comprising:

a) determining a first group of patterns of hybridization products on an array for samples of a first set, wherein each sample within said first set comprises a different collection of fractionated genomic nucleic acid from said member(s), wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence within the genome of said species, wherein hybridization products are formed

between said nucleic acid molecules and said fractionated genomic nucleic acid,

b) determining at least one second group of patterns of hybridization products on said array for samples of at least one second set, wherein each sample within said second set comprises a different collection of fractionated genomic nucleic acid from at least one second member, said second member(s) being different for each second set, and

c) identifying said region based on a comparison between said first and second groups of patterns of hybridization products and the genetic relationship between said member(s) and each second member(s).

52. The method of claim 51, wherein said species is maize.

53. The method of claim 51, wherein said phenotype is a growth characteristic.

54. A method for identifying a region of a genome of a species, said region containing a nucleic acid sequence that contributes to a phenotype observed in a member of said species, said method comprising contacting an array with a first set of samples and at least one second set of samples, wherein each sample within said first set contains a different collection of fractionated genomic nucleic acid from said member, wherein each sample within said second set comprises a different collection of fractionated genomic nucleic acid from a second member, said second member being different for each second set, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within said genome, said contacting being performed such that a first group of patterns of hybridization products is formed for each sample of said first set and a second group of patterns of hybridization products is formed for each sample of said second set, said hybridization products being formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein said region is identifiable based on a comparison between said first and second groups of patterns of hybridization products and the genetic relationship between said member and each second member.

55. A method of genotyping a member of a species, said method comprising determining a pattern of hybridization products on an array for a plurality of samples, wherein each sample contains a different collection of fractionated genomic nucleic acid from said member, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence within the genome of said species, wherein said hybridization products are formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein said pattern indicates the genotype of said member.

56. A method of genotyping a member of a species, said method comprising contacting an array with a plurality of samples, wherein each sample comprises a different collection of fractionated genomic nucleic acid from said member, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within the genome of said species, wherein said contacting is performed such that a pattern of hybridization products is formed for each sample, said hybridization products being formed between said molecules and said fractionated genomic nucleic acid, wherein said pattern for each sample indicates the genotype of said member.

57. A method of genotyping a nucleic acid sample, said method comprising determining a pattern of hybridization products on an array for a plurality of fractions, wherein each fraction comprises a different collection of fractionated genomic nucleic acid from said nucleic acid sample, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence within a genome of a species, wherein said hybridization products are formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein said pattern for each fraction indicates the genotype of said nucleic acid sample.

58. A method of genotyping a nucleic acid sample, said method comprising contacting an array with a plurality of fractions, wherein each fraction comprises a

different collection of fractionated genomic nucleic acid from said nucleic acid sample, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleic acid sequence corresponding to a different sequence within a genome of a species, wherein said contacting is performed such that a pattern of hybridization products is formed for each fraction, said hybridization products being formed between said nucleic acid molecules and said fractionated genomic nucleic acid, wherein said pattern for each fraction indicates the genotype of said nucleic acid sample.

59. The method of claim 58, wherein said nucleic acid sample comprises genomic nucleic acid from a member of said species.

60. The method of claim 58, wherein said nucleic acid sample comprises genomic nucleic acid from more than one member of said species.

61. The method of claim 58, wherein said nucleic acid sample is from a blood sample.

62. A method of producing a genetic map for a species, said method comprising performing amplification reactions on a plurality of samples using a plurality of IDP primer pairs, wherein each sample comprises genomic nucleic acid from a different member of said species, wherein each IDP primer pair amplifies a different nucleic acid region within the genome of said species, wherein each nucleic acid region contains a different IDP, wherein said amplification reactions are performed such that the presence or absence of each different IDP is determined for each sample, and wherein the relationship between each different nucleic acid region within said genome is determinable based on the presence or absence of each different IDP and the genetic relationship of said different members, said relationship being said genetic map.

63. The method of claim 62, wherein said species is a plant species.

64. The method of claim 62, wherein said species is maize.

65. The method of claim 62, wherein said plurality of samples comprises at least five samples.

66. The method of claim 62, wherein said plurality of samples comprises at least ten samples.

67. The method of claim 62, wherein said plurality of IDP primer pairs comprises at least about 500 IDP primer pairs.

68. The method of claim 62, wherein said plurality of IDP primer pairs comprises at least about 1000 IDP primer pairs.

69. The method of claim 62, wherein every twenty-five cM region of said genome contains at least one of said nucleic acid regions.

70. The method of claim 62, wherein every two cM region of said genome contains at least one of said nucleic acid regions.

71. The method of claim 62, wherein said determining the relationship between each nucleic acid region within said genome is determining the relative position of each nucleic acid region within said genome.

72. The method of claim 62, wherein said determining the relationship between each nucleic acid region within said genome is determining the relative distance between each nucleic acid region within said genome.

73. A method for identifying a region of a genome of a species, said region containing a nucleic acid sequence that contributes to a phenotype observed in at least one member of said species, said method comprising:

a) performing a first set of amplification reactions with a sample comprising

genomic nucleic acid from said member(s) and a plurality of IDP primer pairs, wherein each IDP primer pairs amplifies a different nucleic acid region within said genome of said species, wherein each nucleic acid region contains a different IDP, wherein said first set of amplification reactions is performed such that the presence or absence of each different IDP is determined for said member(s), and

b) performing a subsequent set of amplification reactions with at least one subsequent sample and said plurality of IDP primer pairs, wherein each subsequent sample contains genomic nucleic acid from at least one subsequent member of said species, said subsequent member(s) being different for each subsequent sample, wherein said subsequent set of amplification reactions is performed such that the presence or absence of each different IDP is determined for said subsequent member(s), said region being identifiable based on a comparison between the results of said first and subsequent sets of amplification reactions and the genetic relationship between said member(s) and each subsequent member(s).

74. The method of claim 73, wherein said species is maize.

75. The method of claim 73, wherein said phenotype is a growth characteristic.

76. A method of genotyping a member of a species, said method comprising performing a set of amplification reactions with a sample comprising genomic nucleic acid from said member and a plurality of IDP primer pairs, wherein each IDP primer pair amplifies a different nucleic acid region within the genome of said species, wherein each nucleic acid region contains a different IDP, wherein said set of amplification reactions are performed such that the presence or absence of each IDP is determinable for said member, wherein said presence or absence of each IDP indicates the genotype of said member.

77. A method of genotyping a nucleic acid sample, said method comprising performing a set of amplification reactions with said nucleic acid sample and a plurality of IDP primer pairs, wherein each IDP primer pair amplifies a different nucleic acid region within a genome of a species, wherein each nucleic acid region

contains a different IDP, wherein said set of amplification reactions are performed such that the presence or absence of each IDP is determinable for said nucleic acid sample, wherein said presence or absence of each IDP indicates the genotype of said nucleic acid sample.

78. The method of claim 77, wherein said nucleic acid sample comprises genomic nucleic acid from a member of said species.

79. The method of claim 77, wherein said nucleic acid sample comprises genomic nucleic acid from more than one member of said species.

80. The method of claim 77, wherein said nucleic acid sample is from a blood sample.

81. A genotyping method comprising contacting an array with a plurality of samples to form a pattern of hybridization products for each sample, each sample comprising a different collection of fractionated genomic nucleic acid.

82. The method of claim 81, wherein said fractioned genomic nucleic acid is labeled.

83. A method for identifying a nucleic acid sequence that is regulated by a second nucleic acid sequence, said method comprising,

a) determining a first pattern of hybridization product intensities on an array, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence transcribed by a member of a species, said first pattern of hybridization product intensities being formed between a first pool of nucleic acid and said nucleic acid molecules, wherein said first pool of nucleic acid corresponds to mRNA and is obtained from a first group of individuals from said species, wherein said first group of individuals have said second nucleic acid sequence, and

b) determining a second pattern of hybridization product intensities on said array,

said second pattern of hybridization product intensities being formed between a second pool of nucleic acid and said nucleic acid molecules, wherein said second pool of nucleic acid corresponds to mRNA and is obtained from a second group of individuals from said species, wherein said nucleic acid sequence is identifiable based on a comparison between said first and second patterns of hybridization product intensities.

84. The method of claim 83, wherein said first and second groups of individuals are progeny of the same parental cross.

85. The method of claim 83, wherein said first pool of nucleic acid is mRNA.

86. The method of claim 83, wherein said first pool of nucleic acid is labeled.

87. The method of claim 83, wherein said second pool of nucleic acid is mRNA.

88. The method of claim 83, wherein said second pool of nucleic acid is labeled.

89. The method of claim 83, wherein said nucleic acid molecules are expressed sequence tags from said species.

90. A method for identifying a nucleic acid sequence that is regulated by a second nucleic acid sequence, said method comprising contacting an array with first and second pools of nucleic acid, wherein said array comprises a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence corresponding to a different sequence transcribed by a member of a species, wherein said first pool of nucleic acid corresponds to mRNA and is obtained from a first group of individuals from said species, wherein said first group of individuals have said second nucleic acid sequence, wherein said second pool of nucleic acid corresponds to mRNA and is obtained from a second group of individuals from said species, wherein said second group of individuals do not have said second nucleic acid sequence, wherein said contacting is performed such that a first pattern of hybridization product

intensities is formed between said first pool of nucleic acid and said nucleic acid molecules and a second pattern of hybridization product intensities is formed between said second pool of nucleic acid and said nucleic acid molecules, wherein said nucleic acid sequence is identifiable based on a comparison between said first and second patterns of hybridization product intensities.

91. A method for detecting a polymorphism in a member of a species, said method comprising:

a) performing an amplification reaction with genomic nucleic acid from said member and a primer pair such that a product is formed if said genomic nucleic acid contains said polymorphism, and

b) detecting the presence or absence of said product without size-fractionation.

92. The method of claim 91, wherein said polymorphism is an IDP.

93. The method of claim 91, wherein said primer pair is an IDP primer pair.

94. The method of claim 91, wherein said amplification reaction contains a molecule for detection of said product.

95. The method of claim 91, wherein said molecule is ethidium bromide.